

*Anderson et al.
Serial No.: 09/941,626
Page 2 of 8*

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claim 1. (amended) A method for identifying a plurality of infectious particles in a sample comprising:
separating an infectious particle containing fraction,
extracting at least two nucleic acids from the fraction,
sequencing at least a portion of the at least two nucleic acids or a complementary sequence thereof, and
determining the identity of the infectious particles from the sequence or by overlapping sequences derived from plural sequenced nucleic acids.

Claim 2. (original) The method of claim 1 wherein the sample is a mixture of biological samples from plural individuals.

Claim 3. (original) The method of claim 1 further comprising comparing the sequence of the nucleic acids to a database of known sequences.

Claim 4. (original) The method of claim 3 wherein a new infectious particle is detected.

Claim 5. (original) The method of claim 4 wherein a known infectious particle is simultaneously detected.

Anderson et al.
Serial No.: 09/941,626
Page 3 of 8

Claim 6. (original) The method of claim 4 wherein plural new infectious particles are simultaneously detected.

Claim 7. (original) The method of claim 1 wherein the infectious particle is not cultured.

Claim 8. (original) The method of claim 1 wherein the nucleic acids are amplified in copy number between extracting and sequencing.

Claim 9. (original) The method of claim 1 wherein said fraction is separated by centrifugation.

Claim 10. (original) The method of claim 9 wherein the infectious particles band at a density between 1.05 and 1.3 gm/ml and exhibit sedimentation coefficients between 80 and 1,500 S.

Claim 11. (original) The method of claim 1 wherein said fraction is separated by filtration and a retentate is recovered.

Claim 12. (original) The method of claim 1 wherein said at least one nucleic acid is RNA and further comprising synthesizing a DNA complementary to said RNA.

Claim 13. (original) The method of claim 3 wherein the database contains nucleic acid sequences from known infectious particles or the sequences of the species from which the biological sample is obtained.

Claim 14. (original) The method of claim 1 wherein said nucleic acids are cleaved such that overlapping fragments are formed.

Anderson et al
Serial No.: 09/941,626
Page 4 of 8

Claim 15. (canceled).

Claim 16. (original) The method of claim 1 wherein the sample is an aliquot from a composition intended for contacting a living organism.

Claims 17-58. (canceled).

Claim 59. (amended) The method of claims 1, 21, 29, 38, 47, or 49 wherein the method is performed in a containment system.

Claims 60-62. (canceled).

Claim 63. (new) The method of claim 2 wherein the individuals are humans.

Claim 64. (new) The method of claim 9 wherein the centrifugation is performed in a density gradient.

Claim 65. (new) The method of claim 13 wherein the database contains sequences from different unrelated known infectious particles.

Claim 66. (new) The method of claim 1 wherein the samples are not suspected of containing a specific infectious particle.

Claim 67. (new) The method of claim 1 wherein the sequences include at least part of a non-coding sequence of the infectious particle.

Claim 68. (new) The method of claim 1 wherein the sequencing is performed by hybridization to an immobilized oligonucleotide microarray.